Exploring clade differentiation of representative bacterial species in the human gut microbiome (GM) under microgravity conditions

RATING MICROGRAVITY

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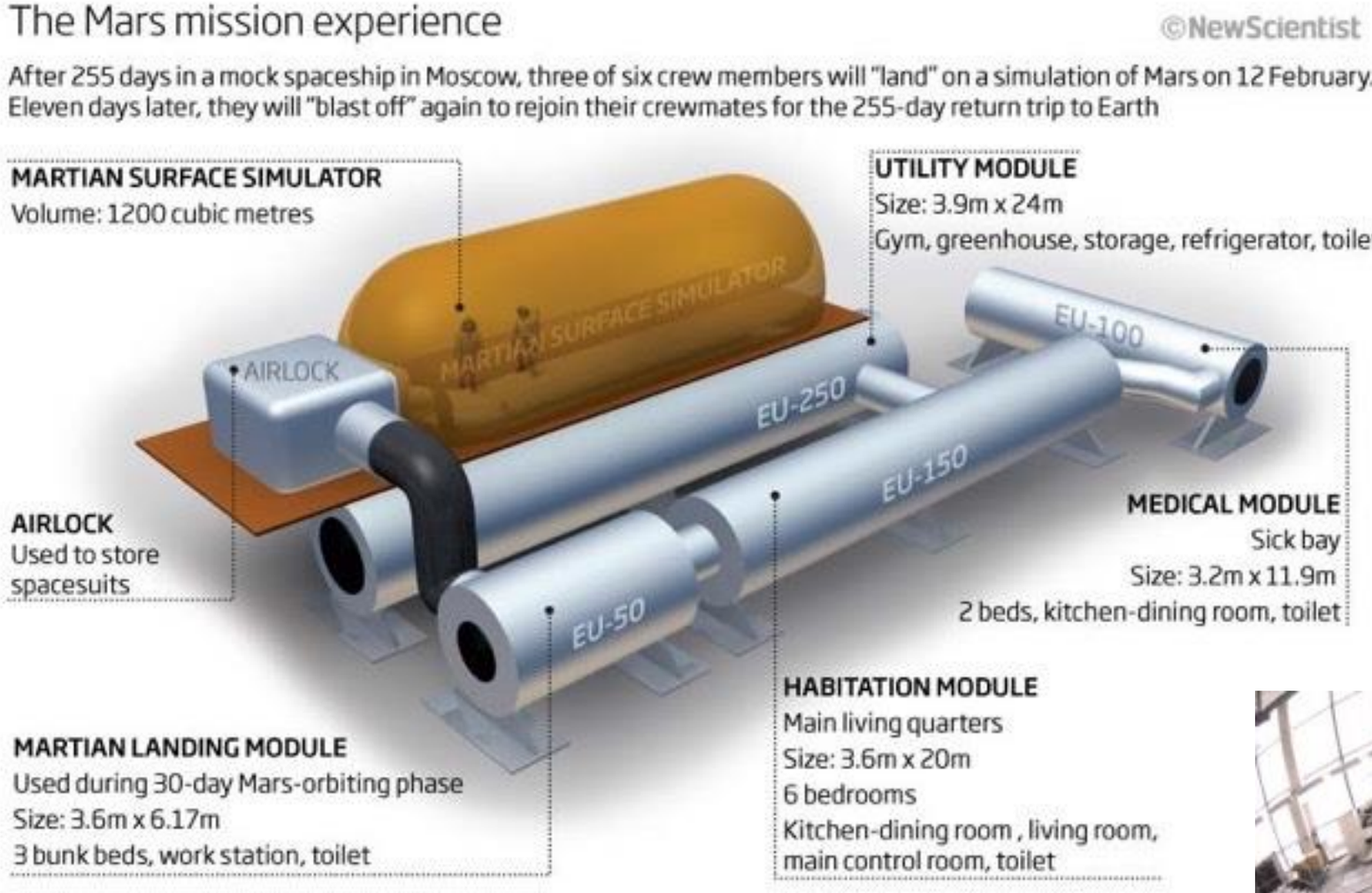
The simulation model for a Martian base

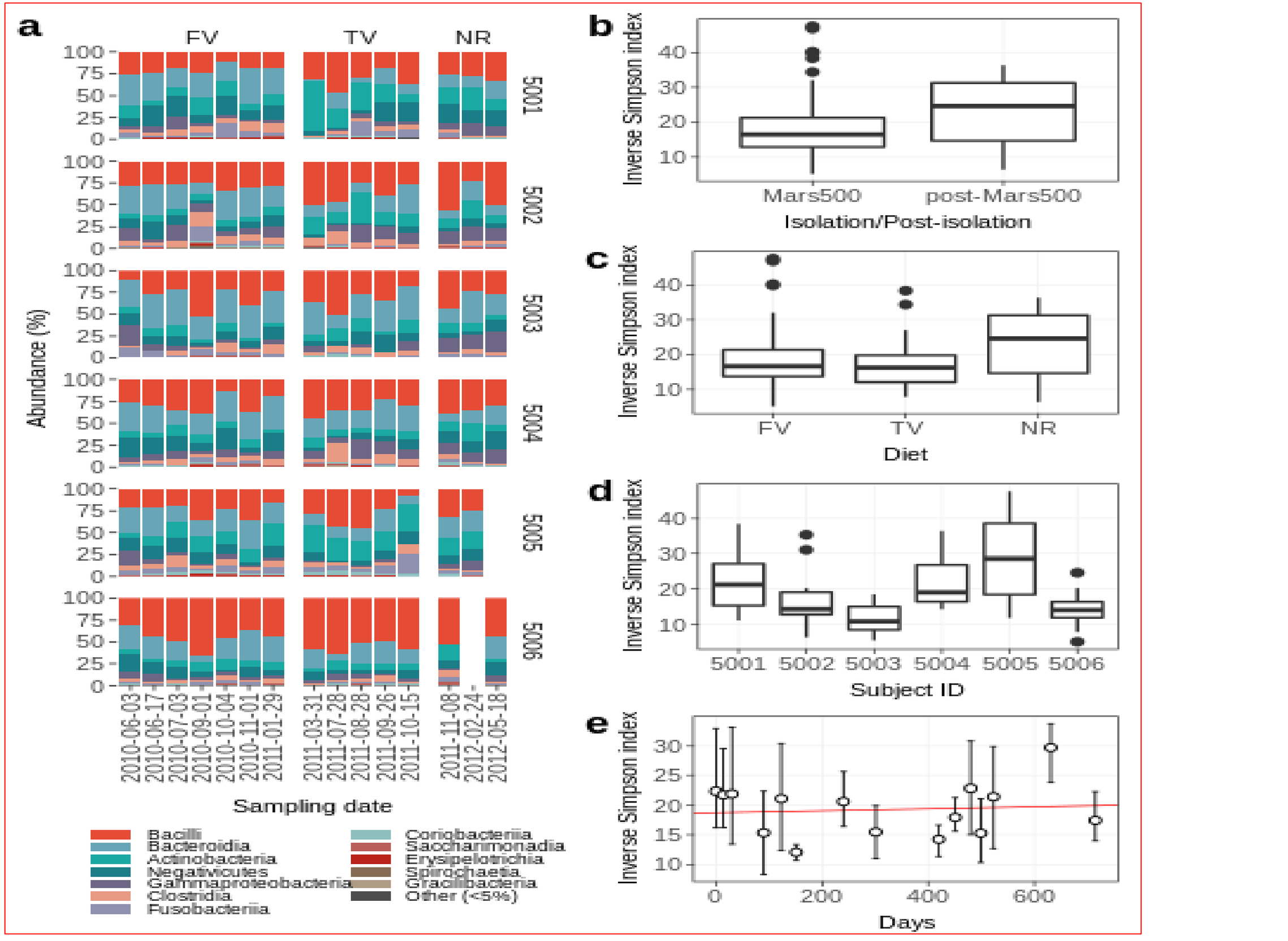


- Located in a special building on the IBMP site in Moscow
- Four hermetically sealed interconnected habitat modules
- One external module, which was used to simulate the 'Martian surface’
- The total volume of the habitat modules is 550 m^3

Schedule and set of the experimental simulation

- Conducted by Russia, the European Space Agency (ESA), and China
- A total of **640 experiment days**
- Started in 2007
- Divided into three stages:
    1. First stage: 15 November 2007 - 27 November 2007 (15 days)
    2. Second stage: 31 March 2009 - 14 July 2009 (105 days)
    3. **Third stage: 3 June 2010 - 4 November 2011 (520 days)**
- During each stage the **6 crew volunteers** lived and worked in a sealed structure which simulated a spaceship
- Communication with the outside word was limited and was conducted with a realistic time delay of up to 25 minutes

Main results (1)



Faecalibacterium prausnitzii, Cristensenella minuta, Bifidobacterium longum

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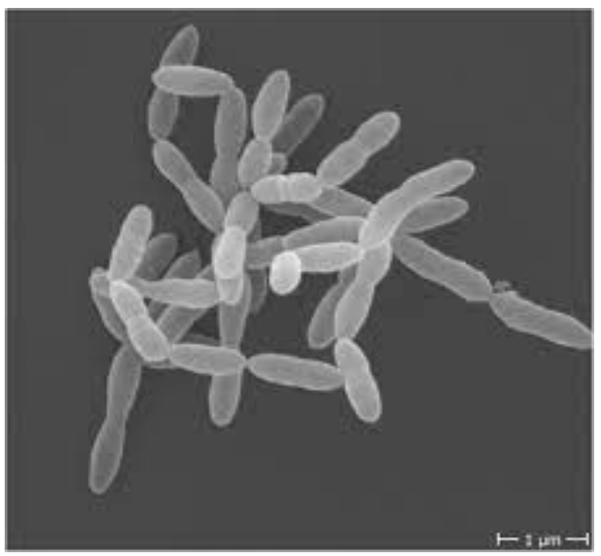
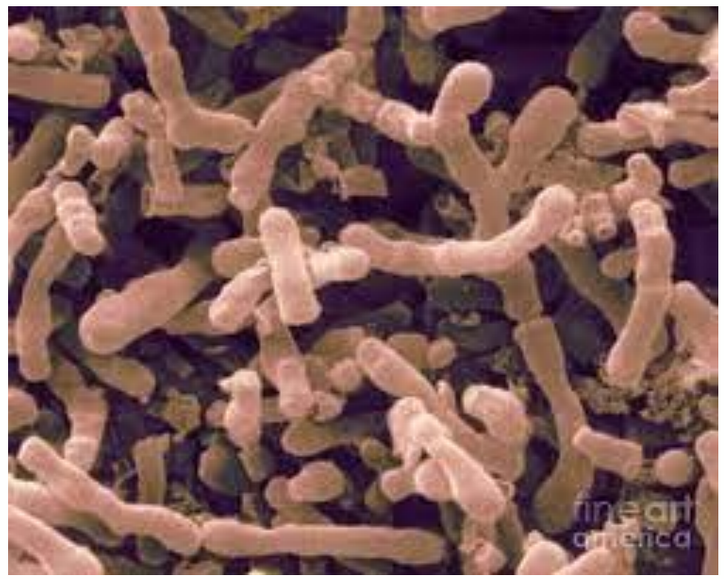
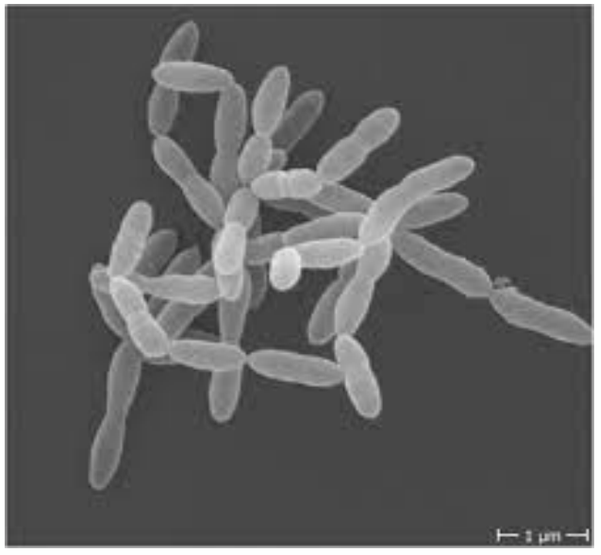
Faecalibacterium prausnitzii, Cristensenella minuta, Bifidobacterium longum are among the most wide-spread and abundant bacteria in the human gut microbiome (GM). They are generally considered as integral components of our evolutionary history which has populated our lineage for at least 1M years. All of them have been consistently reported as the main health-promoting components found in the intestine, showing a crucial role in host nutrition and immunity, where they act as important anti-inflammatory commensals.

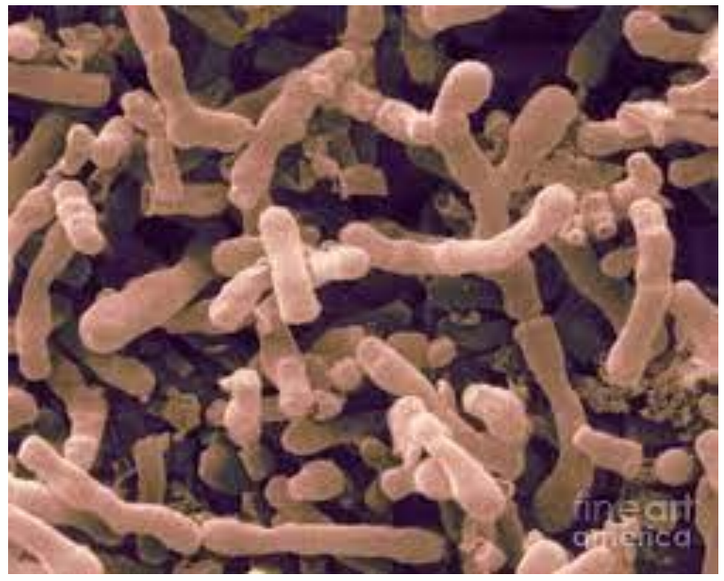




Faecalibacterium prausnitzii, Cristensenella minuta, Bifidobacterium longum

Over the last few years an increasing number of studies have reported a depletion of these species in GMs associated with multiple diseases, enteric and non-enteric, to the point that these bacteria have been defined as biomarkers of a healthy gut. This will probably define a complex scenario where microgravity will play the main stress factor to humans in space, and the clades of the selected GM species will be monitored to get novel insights into their distribution, prevalence or abundance.





Scientific basis and expectations

Phylogenetic analyses is expected to show different *Faecalibacterium prausnitzii, Cristensenella minuta, Bifidobacterium longum* phylogroups (clades) in the human GM, showing different distribution in healthy subjects, according to age, and in patients with gut disorders.

Multiple investigations have confirmed the reduction of clades diversity and abundance in inflammatory bowel disease and obesity. Although these findings certainly represent a milestone for a better understanding of human gut biology, there is still few evidence concerning possible selective pressures driving for clades divergences in human populations, as well as for the drivers forcing their depletion in disease setting, and no information are available about the clades response to long exposure to microgravity, in connection with health.

Experimental model

- We would like to explore the response of *Faecalibacterium prausnitzii, Cristensenella minuta, and Bifidobacterium longum* phylogroups clades in term of abundance, diversity and dynamics involved in the divergence processes of the clade-specific marker genes in to long exposure to microgravity.

- Our aim will be dissecting the peculiarities of each clade and providing some glimpses on the putative in-flight pressures selectively acting on each of them.

- We will reconstruct high-quality genomes from metagenomes (MAGs) starting from ~750 healthy human gut metagenomes and identified all clades by implementing previously validated pipelines. Then, the within-clade genetic diversity of astronauts will be analyzed in different time-points during pre-flight, post-flight and in flight, allowing to dissect clades variations and the putative evolutionary forces acting on each clade.

- The divergence dynamics will be assessed by accounting for the specific pattern of mutations accumulating in the respective clade-specific genes. Given the high susceptibility of this species to alteration of host homeostasis and environmental stresses, our findings may provide new insights into the determinants responsible for its decrease under microgravity conditions and help to find solutions to sustain human health in space.

Partners in the present research proposal

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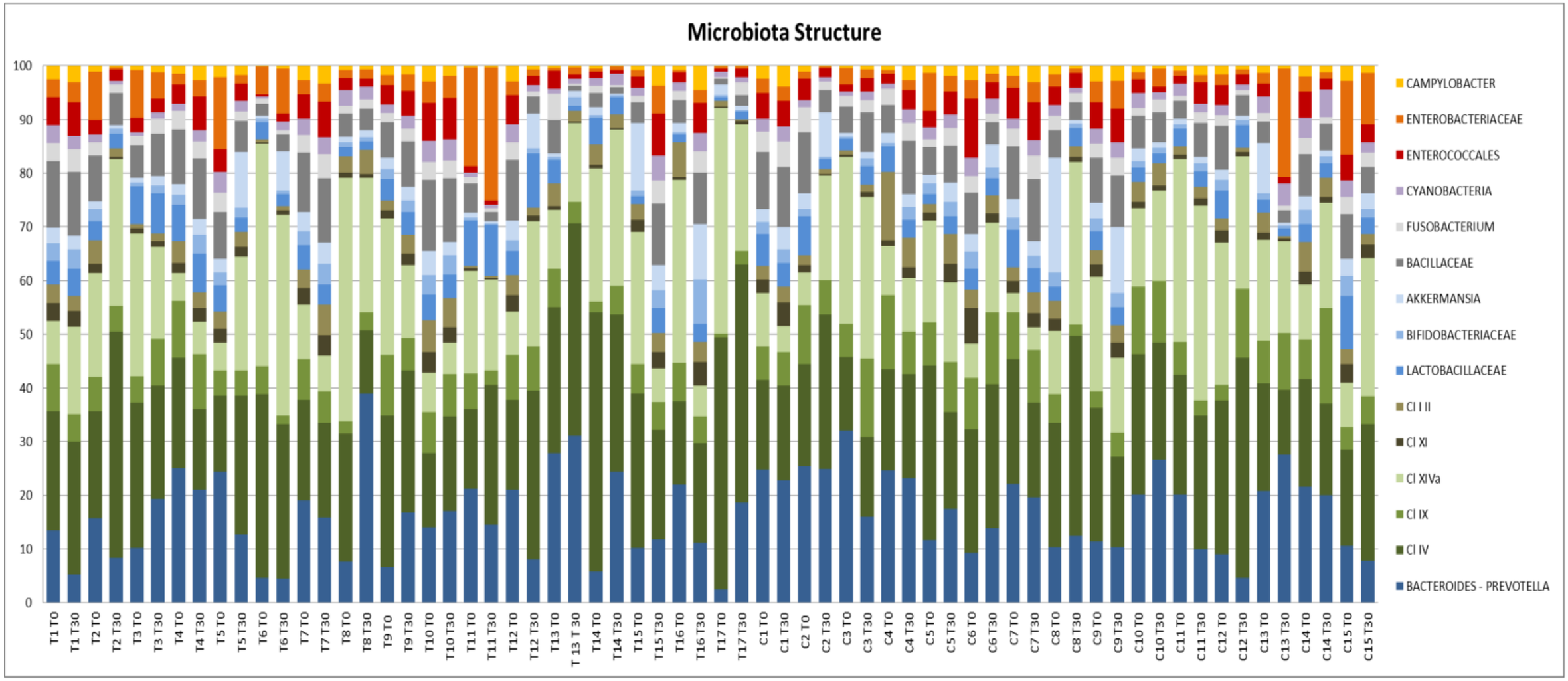
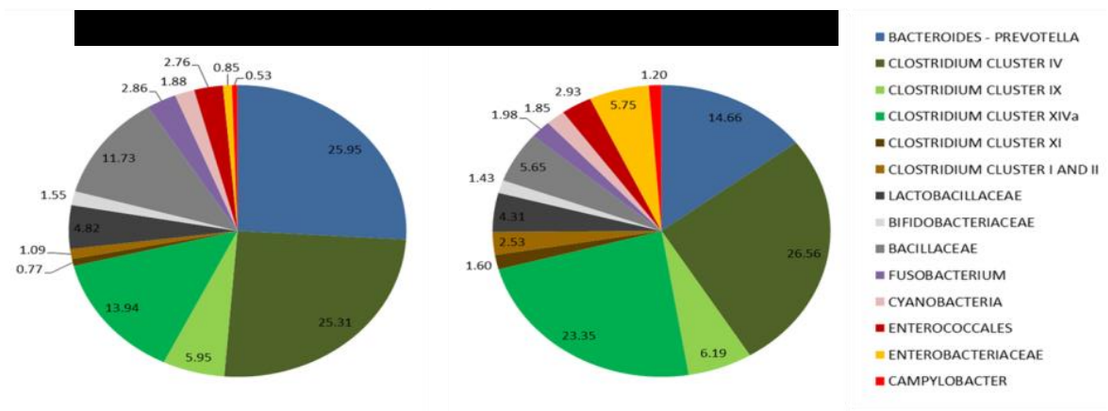
Characterization of the fecal microbiota and individual clusters





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Model of experimental timing for sampling before, during and after flight mission